

Figure 1(a)

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HHV8PEP      -----MTPRSR-LATLGTVILLVCFAG--AAHSRGDTFQ--
RHESRHADPEP -----MMITNRTRLLRAWVVI IAGTAVG--ENVTTPKGAT--
MURH68PEP    -----MYPTVKSMRVAHLTNLLTLLCLLCHTHLYVCQPTTLR--
BOVINEH4PEP  YYKTILFFALIKVCSFNQTTTHSTTTTSPSISSTTSSTTSTSKPSNTTSTNSSLAASPQ
ATELINEH3PEP -----MTLNR---CVLLIVLTFSTACS-----Q--
SAIMIRIPEP   -----MVPNK---HLLLIILSFSTACG-----Q--
EQH2PEP      -----MGVGGGPRVVLCCLWCVAALLCQGVAEVVAETTTTFFA--
EQH5PEP      -----MVAWFGLWGFARLMATLALLCGRVALDESSATPSIPP--
ALCELPEP     -----MAHTGSTVCAFLIFAVLKNVFCQPTPTSSEVEDVIPEAN-
EBVPEP       -----MTRRRVLSVVVLLAALACRLGA-----Q--TPEQ--

HHV8PEP      --TSSSPTPPGSSSKAPTCKPGEASGPKSVDFYQFRVCSAS-ITGELFRFNLEQTCPTDK
RHESRHADPEP  --TTAKPTP-GPS--TPTPP---ENPPR-AEAFKFRVCSAS-ATGELFRFNLEKTCPGTE
MURH68PEP    --QPSDMTP-AQDAPTETPPPLSTNTNR--GFEYFRVCGVA-ATGETFRFDLDKTCPTQ
BOVINEH4PEP  NTSTSKPSTDNQGTSTPTIPTVDDTAS-KNFYKYRVCSSSSSGELFRFDLDQTCPTDK
ATELINEH3PEP ----TTPASSDEN--GKTPAIEK--EYF----K-YRVCSAS-TTGELFRFNLDRACPSTE
SAIMIRIPEP   ----TPTTAVEK--NKTQAIYQ--EYF----K-YRVCSAS-TTGELFRFDLDRTCPSTE
EQH2PEP      ---THRPEVVAEE--NPANP-----FLP----F--RVCGASPTGGEIFRFPLEESCNPTE
EQH5PEP      ---THKPAVHHED--NTTNP-----FLL----F--RVCGASPTG-EIFRFPLEENCNPTE
ALCELPEP     --TVSDNIIRQOR--NNTAKGIHSDPSA----FPFRVCSAS-NIGDIFRQTSHSNCPNTK
EBVPEP       ---PAPPATTVQP--TATRQ-----QTS----FPFRVCELS-SHGDLFRFSSDIQCPSTF

HHV8PEP      DKY-HQEGILLVYKKNIVPHIFKVRRYRKIATSVTVYRGLTES--AITNKYELPRVPPLY
RHESRHADPEP  DKT-HQEGILMVFKKNIVPHIFKVRRYRKVATSVTVYRGWTET--AVTGKQEVIRPVPQY
MURH68PEP    DKK-HVEGILLVYKINIVPYIFKIRRYRKIIITQLTIWRGLTTS--SVTGKFEMATQAHEW
BOVINEH4PEP  DKK-HVEGILLVLKKNIVPYIFKVRKYRKIATSVTVYRGWSQA--AVTNRDDISRAIPYN
ATELINEH3PEP DKV-HREGILLVYKKNIVPHIFKVRYYKKIATSVRIFNGWSREGVAITNKWELSRAPKY
SAIMIRIPEP   DKV-HKEGILLVYKKNIVPYIFKVRYYKKITTSVRIFNGWTREGVAITNKWELSRAPKY
EQH2PEP      DKD-HIEGIALIYKTNIVPYVFNVRKYRKIMTSTTIYKGWSED--AITNQHTRSYAVPLY
EQH5PEP      DKE-HVEGILLIYKTNIVPYIFNVRKYRKLVSTSTTIYKGWSQD--AITNQYTSFAMPLW
ALCELPEP     DKE-HNEGILLIFKENIVPYVFKVRKYRKIVTTSTIYNGIYAD--AVTNQHVFSKSVPIY
EBVPEP       TRENHTEGLLMVFKDNIIPYSFKVRSYTKIVTNILIYNGWYAD--SVTNRHEEKFSVDSY

HHV8PEP      EISHMDSTYQCFSSMKVNVNGVENTFTDRDDVNTTVFLQPVEGLTDNIQRYFSQPVIYAE
RHESRHADPEP  EINHMDTTYQCFSSMRVNVNGIVNTYTDRDFTNQT VFLQPVEGLTDNIQRYFSQPVLYTT
MURH68PEP    EVGDFDSIYQCYNSATMVVNNVRQVYVDRDGVNKT VNI RPDGLTGNIQRYFSQPTLYSE
BOVINEH4PEP  EISMIDRTYHCFSAMATVINGILNTYIDRDSENKSVPLQP VAGLTENINRYFSQPLIYAE
ATELINEH3PEP EINLMDKNYQCHNCMQIEVNGLLNSYCDRDGNNKT VDLKPVDGLTGAITRYVSQPKIFAD
SAIMIRIPEP   EIDIMDKTYQCHNCMQIEVNGMLNSYDRDGNNKT VDLKPVDGLTGAITRYISQPKVFAD
EQH2PEP      EVQMMDHYYQCFSAVQVNEGGHVNTYVDRDGWNETAFLKPADGLTSSITRYQSQPEVYAT
EQH5PEP      EARLVDYNYECYNGIQVTENGHLTTYVDRDGYNESVRLVPADGLTSSIRRYHSQPELYVT
ALCELPEP     ETRRMDTIYQCYNSLDVTVGGNLLVYTDNDGSNMTVDLQPV DGLSNSVRRYHSQPEIHAE
EBVPEP       ETDQMDTIYQCYNAVKMTKDGLTRVYVDRDGVNITVNLKPTGGLANGVRRYASQTELYDA

HHV8PEP      PGWFPGIYRVRTTVNCEIVDMIARSAEPYNYFVTSLGDTVEVSPFCYNSSCST-TPSNK
RHESRHADPEP  PGWFPGIYRVRTTVNCEIVDMIARSAEPYSYFVTALGDTVEVSPFCHNDSTCSV-AEKTE
MURH68PEP    PGWMPGFYRVRTTVNCEIVDMVARSMDPYNYIATALGDSLELSPFQTFDNTSQS-TAPKR
BOVINEH4PEP  PGWFPGIYRVRTTVNCEIVDMYARSVEPYTHFITALGDTIEISPFCHNNSQCTTGNSTSR
ATELINEH3PEP AGWLWGTYKTRRTTVNCEIVEMFARSADPYTYFVTALGDTVEVSPFCDAENSCPN----AS
SAIMIRIPEP   PGWLWGTYRTRRTTVNCEIVDMFARSADPYTYFVTALGDTVEVSPFCVDVNSCPN----AT
EQH2PEP      PRNLLWSYTTRTTVNCEIVTEMSARSMKPFVFTSVGDTIEMSPFLKENGTEPE--KILK
EQH5PEP      PRNLLWSYTTRTTVNCEIVDMTARSHKPFYFVTASGDSIETSPFYT-NASR-----R
ALCELPEP     PGWLLGGYRRRTTVNCEIVTETDARAVPPFRYFITNIGDTIEMSPFWSKAWNETEFS--GE
EBVPEP       PGWLIWTYRTRRTTVNCEITDMMAKSNSPFDFVTTTGQTVEMSPFYDGKNKETF----HE

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Figure 1(b)

HHV8PEP	NGLSVQVVLNHTVVVTYSDRGTSPTPQNRIFVETGAYTLWSASESKTTAVCPALALWKTFFPR
RHESRHADPEP	NGLGARVLNTYTMVDFATR--APTETRVFADSGEYTVSWKAEDPKSAVCALTLWKTFFPR
MURH68PEP	ADMVRREVKNYKFVDYNNRGTAAGQSRTFLETSPATYSWKTATRQTATCDLVHWKTFFPR
BOVINEH4PEP	DATKVVIEENHQTVDYERRG-HPTKDKRIFLKDDEEYTLISWKAEDRERAICDFVIWKTFFPR
ATELINEH3PEP	DVLSSQVDFNHTVVVDYGNRATSQQHKGKRIFAHTLDYSVSWEAINKTTSVCSMVFWKGFQR
SAIMIRIPEP	DVLSVQIDLNHTVVVDYGNRATSQQHKKRIFAHTLDYSVSWEAVNKSASVCSMVFWKSFQR
EQH2PEP	RPHSIQLLKNYAVTKYGVGLGQADNATRFFAIFGDYSLSWKATTENSZYCDLILWKGFNS
EQH5PEP	VP--VQVLYNYSVTYDYGVLGSGENVTRFFATLNDFSISWKAATENSZYCPLVLWKGFPS
ALCELPEP	PDRTLTVAKDYRVVDYKFRGTQPGHTRIFVDKBEYTLWSAQQFRNISYCRWAHWSFDN
EBVPEP	RADSFHVRTNYKIVDYDNRGTNPQGERRAFLDKGTYTLWSKLENR-TAYCPLQHWQTFDS
HHV8PEP	SIQTTTHEDSFHFVANEITATFTAP---LTPVANFTDTYSCLTSDINTTLNASKAKLASTH
RHESRHADPEP	AIQTTHEASYHFVANDVTATFTSP---LSEVANFTGTYSCLDEVIQKTLNDTIKKLSDTH
MURH68PEP	AIQTAHEHSYHFVANEVTATFTNP---LTEVENFTSTYSCVSDQINKTISEYIQLNNSY
BOVINEH4PEP	AIQTIHNESFHFVANEVTASFLTSNQEETELRGNTEILNCMNSTINETLEETVKKFNKSH
ATELINEH3PEP	AIQTEHDSTYHFIANEITAGFSTS---KETLASFSSEYSCLMSDINSTLTDKIGRVNNTH
SAIMIRIPEP	AIQTEHDLTYHFIANEITAGFSTV---KEPLANFTSDYNCLMTHINTTLEDKIARVNNTH
EQH2PEP	AIQTQHNSSLHFIANDITASFSTP---LEEEAN-FNETFKCIWNNTQEEIQQKLEVEKTH
EQH5PEP	AIQTKHEKSYHFIAADAVTASFTTP---LTDETSYFNNTTYQCAWQDIEGEIQKRFDPVSKTH
ALCELPEP	AIKTEHGKSLHFVANDITASFYTP---NTQTREVLGKHVCLNNTIESELKSLAKVNDTH
EBVPEP	TIATETGKSIHFVTDEGTSSFVTN---TTVGIELPDAFKCIEEQVNKTMHEKYEAVQDRY
HHV8PEP	VP-NGTVQYFHTTGGLYLWVQPMASAINLTHAQ-GDSGNPTSSPPPSASP-----M
RHESRHADPEP	VT-NGSAQYKTEGGLFLLWQPLTPLSLVDEMRLNG---TTPAP---P-----A
MURH68PEP	VA-SGKTQYFKTDGNLYLIWQPLEHPEIEDID--EDSDPEPTAP---P-----K
BOVINEH4PEP	IR-DGEVKYKTNGLFLIWAQAMKPLNLSEHT-----N-YTIER---N-----N
ATELINEH3PEP	VP-NGTAQYFKTEGGMILWVQPLTAIELEEAMIEATTVSPTPLS-----T
SAIMIRIPEP	TP-NGTAEYYQTEGGMILWVQPLIAIELEEAMLEATTSPVTPSAP-----T
EQH2PEP	RP-NGTAKVYKTTGNLYIYVQPLIQIDLLDTHAKLYNLTNATASPTSTP-----
EQH5PEP	AR-NGSVQIYKTSNLYVWQPLVQLDLLAAHAKTINSTDNSTSPPTAPN-----TT
ALCELPEP	SP-NGTAQYLLTNGGLLLWVQPLVQKLLDAKGLLDVAVKKQNTTTT-----T
EBVPEP	TKGQEAITYFITSGLLLAWLPLTPRSLATVKNLTELTTPTSSPPSSPSPAPSARGST
HHV8PEP	TTSASRRKRRSASTAAAGG---GGSTDN-----LSYTQLOQFAYDKLRDGINQVLEELSRA
RHESRHADPEP	TTSTVSRVRRSVNTNEQ-----ATDN-----LAAPQLOQFAYDKLRASINKVLEELSRA
MURH68PEP	STRKKREAADNGNSTSEVS---KGSNP-----LITAQIQFAYDKLTTSVNNVLEELSRA
BOVINEH4PEP	KTGNKSRQKRSVDTKTFQG-----AKG-----LSTAQVQYAYDHLRTSMNHILEELTKT
ATELINEH3PEP	AHLTSRRTGRRKRDVSAG-----SENS-----VLLAQIQYAYDKLRQSINNVEELAIT
SAIMIRIPEP	SSSRSKRAIRSIRDVSAG-----SENN-----VFLSQIQYAYDKLRQSINNVEELAIT
EQH2PEP	-TTSPPRRRRRTSSVSGGG---NNGDNSTKEESVAASQVQFAYDNLRSINRVLGELSRA
EQH5PEP	TSTSSRRKRRDTGNTATNN---SSSNNSSMEENLATSQVQFAYDQLRKSINRVLEQLSRV
ALCELPEP	TTTRSRRQRSSVSSGIDDV---YTAEST-----ILLTQIQFAYDTLRAQINNVEELSRA
EBVPEP	PAAVLRRRRRDAGNATTPVPPTAPGKSLGTLNPNPATVQIQFAYDSLRRQINRMLGDLARA
HHV8PEP	WCREQVRDNLMWYELSKINPTSVMTAIYGRPVSAKFVGDAISVTECINVDQSSVNIHKSL
RHESRHADPEP	WCREQVRDTYMWYELSKINPTSVMTAIYGRPVSAKFVGDAISVTDCAVDQASVSIHKSL
MURH68PEP	WCREQVRDTLMWYELSKVNPTSVMSAIYGKPVAAARYVGDAISVTDICIYVDQSSVNIHQSL
BOVINEH4PEP	WCREQKDNLMWYELSKINPTSVMSAIYGKPVAVKAMGDVAFMVSECINVDQASVNIHKSM
ATELINEH3PEP	WCREQVRQTMWYELIAKINPTSVMTAIYGKPVSAKALGDVIVTECINVDQTSVSIHKSL
SAIMIRIPEP	WCREQVRQTMWYELIAKINPTSVMTAIYGKPVSRKALGDVIVTECINVDQSSVSIHKSL
EQH2PEP	WCREQYRASLMWYELSKINPTSVMSAIYGRPVSAKLIGDVVSVSDCISVDQKSVFVHKNM
EQH5PEP	WCQNQYRASLMWYELSKINPTSVMSAIYGRPVSAKLIGDVVQISDCITVDQESVVFVHRNL
ALCELPEP	WCREQHRASLMWNELSKINPTSVMSIYGRPVSAKRIGDVIVSHCVVVDQDSVSLHRSM
EBVPEP	WCLEQKRQNMVLRBELTKINPTTVMSIYGKAAAKRLGDVIVSVQCPVNPQATVTLRKSM

Figure 1(c)

HHV8PEP
RHERHADPEP
MURH68PEP
BOVINEH4PEP
ATELINEH3PEP
SAIMIRIPEP
EQH2PEP
EQH5PEP
ALCELPEP
EBVPEP

RTN---SKDVCYARPLVTFKFLNSSNLTGQLGARNEIILTNNQVETCKDTCEHYFITRN
RTS---TPGMCYSRPPVTFRFLNSTTLFKGQLGPRNEIILTNDQVEACKETCEHYFIASN
RLQH---DKTTCYSRPRVTFKFINSTDPLTGQLGPRKEIILSNTNIECKDESEHYFIVGE
RTD---DPKVCYSRPLVTFKFVNSTATFRGQLGTRNEILLTNTHVETCRPTADHYFFVK
KTT---NNDVCYSRPPVTFKFVNSSQLFKGQLGARNEILLSESLVENCHQNAEHFFTA
KTE---NNDICYSRPPVTFKFVNSSQLFKGQLGARNEILLSESLVENCHQNAETFFTA
KVPG---KEDLCYTRPVVGFKFINGSELFAGQLGPRNEIVLSTSQVEVCQHSCEHYFQAGN
RVPG---SKDLCYTRPVVGFKFINGSELFVQQLGARNEILLSTNLVEVCQHSCEHYFQGGN
RVPGRDKTHECYSRPPVTFKFINDSHLYKGQLGVNNEILLTTTAVEICHENTEHYFQGGN
RVPG---SETMCYSRPLVSFSFINDTKTYEGQLGTDNEIFLTKKMTEVCQATSQYYFQSGN

HHV8PEP
RHERHADPEP
MURH68PEP
BOVINEH4PEP
ATELINEH3PEP
SAIMIRIPEP
EQH2PEP
EQH5PEP
ALCELPEP
EBVPEP

ETLVYKDYAYLRTINTTDTISLTNFIALNLSFIQNIIDFKAIELYSSAEKRCLASSVFDLET
VTYYYKDYVFKKINTSEISTLGTFIALNLSFIENIDFRVIELYSRAEKKLSGVSVDIET
YIYYKDYIFEEKLNLSIATLDTFIALNLSFIENIDFKTVELYSSTERKLASSVFDIES
MTHYFKDYKFKVKTMDTNNISTLDTFLTLNLTFDIDNIDFKTVELYSETERKMAS-ALDLET
ETYHFKNYLHVETLPLTNISTLDTFLALNLTFIENIDFKAVELYSSGERKLAN-VFDLET
ETYHFKNYVHVETLPLNNISTLDTFLALNLTFIENIDFKAVELYSSGERKLAN-VFDLET
QMYKYKDYVYSTLNLDTIPTLHTMITLNLSTVENIDFKVIELYSKTEKRSLN-VFDIET
HIYKYKDYVYSTMLNLTDPVTLHTMITLNLSTVENIDFQVIQLYSQEKKLSN-VFDIET
NMYFYKNYRHVKTMPVGDVATLDTFMVLNLTVENIDFQVIELYSREKRMST-AFDIET
EIHVYNDYHHFKTIELDGIATLQTFISLNTSLIENIDFASLELYSRDEQRASN-VFDLEG

HHV8PEP
RHERHADPEP
MURH68PEP
BOVINEH4PEP
ATELINEH3PEP
SAIMIRIPEP
EQH2PEP
EQH5PEP
ALCELPEP
EBVPEP

MFREYNYTTHRLAGLREDLNTIDMNERFVRDLSEIVADLGGIGKTVNVASSVVTLCG
MFREYNYTQRLAGLREDLNTIDLNDRDLARDLSEIVADLGDVGRTVNVASSVITLFG
MFREYNYTYSLAGIKKDLNTIDYNDRDLVQDLSMDLGDIGRSVNVVSSVVTFFS
MFREYNYTQKLASLREDLNTIDLNDRDLVKDLSEMMADLGDIGKVVNTFSGIVTVFG
MFREYNYAQSISGLRKDFDNSQRNDRDRIIQDFSEILADLGSIGKVIIVNIASSAFSLFG
MFREYNYAQSISGLRKDFDNSQRNDRDRIIQDFSEILADLGSIGKVIIVNVSAGAFSLFG
MFREYNYTQNLNGLRKDLDDSIDHGRDSFIQTLGDMQDLGTIGKVVNVASGVFSLFG
MFREYNYTQNLKGLRKDLDDSIDHGRDSFIQFLGDLVQDLVPVGDVIVNVASGVFSLFG
MFREYNYTQRTVGLRRDLTD-LATNRNQFVDAGFSLMDDLGVVGKTVLNAVSSVATLFS
IFREYNFQAQNIAGLRKDLDNAVSNRQNFVDGLGELMDSLGSVGSITNLVSTVGGFLS

HHV8PEP
RHERHADPEP
MURH68PEP
BOVINEH4PEP
ATELINEH3PEP
SAIMIRIPEP
EQH2PEP
EQH5PEP
ALCELPEP
EBVPEP

SLVTGFINFIKHPGLGMLMIIIVIAIILIFMLSRRTNTIAQAPVKMIYP---DVDRRA
SIVSGFINFIKSPFGGMLMILVIVAVVLIVFALNRRNTAIAQAPIRMIYP---DIDKMQ
SIVTGFIKFFTNPLGGIFILLIIGGIIFLVVVLNRRNSQFHDAPIKMLYPSVENYAARQA
SIVGGFVSFFTNPIGGVTIILLVVVVFVVFIVSRRTNNMNEAPIKMIYP---NIDKAS
GIVTGILNFIKNPLGGMFTFLLVGAIILVILLVRRTNMNSQAPIRMIYP---DIEKSR
GIVTGILNFIKNPLGGMFTFLLVGAIILVILLVRRTNMNSQAPIRMIYP---DVEKSK
SIVSGVISFFKNPFGGMLLIVLIAGVVVVLVFMTRSRISIYAPIRMLYP---GVERAA
SIVSGVISFLKNPLGAILTIALIVGGIIVLYLFITRSRTVYQAPIRMLYP---EVDRA
SIVSGIINFIKNPFGGMLLFLGLIAAVVITVILLNRKAKRFAQNPVQMIYP---DIKTIT
SLVSGFISFFKNPFGGMLLIVLVAGVVILVISLTRRTRQMSQPVQMLYP---GIDELA

HHV8PEP
RHERHADPEP
MURH68PEP
BOVINEH4PEP
ATELINEH3PEP
SAIMIRIPEP
EQH2PEP
EQH5PEP
ALCELPEP
EBVPEP

PP-----SGGAPTREEIKNILLGMHQLQQ---ERQKADDLKKSTPSVFQRTANGLR
P-----SGGKVDQEQIKNILAGMHQLQQ---EERRRLDEQORSAPSLFRASDGLK
PPPYSA---SPPAIDKEEIKRILLGMHQLVHQ---EEKEAQQLTNSGPTLWQATGFLR
EQE-----NIQPLPGEEIKRILLGMHQLQQ---SEHGKSEEEASHKPGFLQLGDLQ
S-----SVTPTEPEVIKQILLGMHNMQQ---EYKKEEHKASQPSFLKRATDAFL
S-----TVTPMEPETIKQILLGMHNMQQ---EAYKKKEEQRAARPSIFRQAAETFL
QEP-----GAHPVSEDQIRNLMGMHGFQQRQRAEEEARREEVKGKRTLFEVIRDSAT
QQ-----NVQPIPEDQVRSILLAMHGFQQQQQQQQQQQEHTQ-RRSIFDTIRESTS
SQREEL---QVDPISKHELDRIMLAMHDYHASK---QPESKQDEEQGSTTSGPADWLNKAK
QQHASGEGPGINPISKTELQAIMLALHEQNQ-----EQKRAAQRAAGPSVASRALQAAR



ATGGCAGGTA	GCTTAAAACT	TAGGGGATCT	GTTCTAGCAC	TGTGGTACCT	GTATCAGGTG	60
GCTCTTTATT	CACTTAGTAT	AGCAGAGACC	GGTGTAACTT	CACCTCCAAA	TACAGCGACC	120
TGGTCTACTG	AATCGCCGCT	AACAGGTCAC	TATGGAACAC	ACGATTCAAG	CCATGGTGAA	180
AGAGGAAACA	ACGAAAACAG	AGATTCAGAA	GAGCAAAATA	AAAACATTTA	TGGATCGCCT	240
TCTACGTTTC	CTTACAGAGT	ATGCAGTGCC	TCCGGAGTTG	GAGATGTCTT	TAGATTTTCA	300
ACCGACCATG	TGTGTCCCGA	TGCCAGTGAT	ATGGTACACA	GTGAGGGGAT	TCTACTAATT	360
TACAAACAGA	ACATTATTCC	ATTTATGTTT	AGAGTTAGGA	AATATAGAAA	AGTTGTTTACA	420
ACAAGTACTG	TCTACAATGG	TATTTATTCT	GACTCTATTA	CCAACCAACA	TACTTTCTAT	480
AAATCAATCG	AACTTGGGA	GACAGAAAAG	ATGGACACAA	TATATCAGTG	TTTTAATTCT	540
TTAAGACTAA	ACACAGGTGG	AAATCTGCTT	ACTTATGTAG	ATAGAGATGA	TATAAATATG	600
ACAGTGTTC	TGCAACCTGT	TGACGGTGTG	ACGCCCCGAT	TGAAGAGGTA	TGGCAGTCAA	660
CCAGAGCTGT	ACCTTGAACC	TGGCTGGTTT	TGGGGTAGTT	ATAGAAGACG	AACTACAGTG	720
AACTGTGAAC	TAATGGACAT	GTTTGCAAGA	TCAAATCCTC	CATTTGATTT	CTTTGTTTACA	780
GCTACAGGTG	ATACGGTGGA	AATGTCTCCA	TTTTGGAGTG	GTGAAGATGA	TCATGAAAAAT	840
AAGATGCACG	AGAAGCCATG	GTTTGTTAGT	GTGATAAATA	ACTACAAGGT	GGTGGAATAT	900
CAAAACAGAG	GGACTGTACC	CCTTGGAAAA	ACAAGGATAT	TTCTAGATAG	GGGAAGAGTAT	960
ACATTATCTT	GGGAAAAGCA	TCTAAAAAAT	ATGTCATATT	GTCCACTAAC	ATTATGGAAA	1020
GCATTTTACA	ATGGAATCCA	GACGGAGCAT	TCAGGCTCAT	ATCATTTTGT	AGCCAATGAC	1080
ATCACAGCGT	CATTCACAAC	TAGTAAAGAA	GACATGAAAG	AGTTCAATAC	GACATATCAT	1140
TGTCTCAACG	AGGAAATAAA	GGCAGAAATA	GAGAAGAAAT	ATGCAAAAGT	AAACTCAACT	1200
CACTCTAAAT	ATGGAGATCT	GAAATACTTT	AAAACAGATG	GGGGTCTCTA	TTTAGTCTGG	1260
CAACCTCTTA	TTCAAAACAG	GCTTCTTGAT	GCTAAGAACA	AACTGAACAA	TGAGACTTAT	1320
TCCAGGAGAT	CACGACGTCA	GGCAGAATCT	ACTACTGACC	CAGTGTGGA	GGTGACTTGA	1380
AATGGAGCAG	GTGGAGAATA	TAGCAGTGAA	AATCAATCA	CAATGGCGCA	GATGCAGTAT	1440
GCCTATGACA	ATCTTCGTAT	CAGAATAAAT	AAATTTTGG	AAGATTTGTC	AAAGGCATGG	1500
TGTCGTGAGC	AGCATAGAGC	TGCTCTGGTG	TGGAATGAGC	TCAGCAAGAT	TAATCCCA	1560
AGCGTCATGA	GCATGATTTA	CAATAGACCC	GTATCAGCCA	AAAGAATAGG	AGATGTCATT	1620
TCAGTCTCTA	ACTGTATTGT	GGTAGACCAA	ACCAGTGTCT	CATTACATAA	AAGTCTCAGG	1680
CTTCTCAGTG	CATCGGATGA	AAAGTGCTTC	TCTAGACCTC	CAGTGACATT	TAAGTTTATG	1740
AATGACAGTA	CTATTTTACAA	AGGGCAACTA	GGAGTCAATA	ATGAGATTCT	CTTAACCACA	1800
ACATACCCTG	AAACATGTCA	GGAAAACACT	GAGTATTACT	TTCAGGCAAA	GACAGACATG	1860
TACATTTTACA	AAAACATATGA	GCATTTGAAG	ACTGTGCCTT	TATCTTCGAT	CACCACTA	1920
GATACATTTA	TAGCCCTTAA	TTTTACATA	TTGGAGAATG	TTGACTTTAA	AGTCATTGAA	1980
CTTTATACCA	GGGACGAGAA	GAGGCTTAGT	AATGTCCTTG	ACATTGAAAC	AATGTTTAGG	2040
GAATATAACT	ACTATGCTCA	GAGGGTCAGT	GGCCTCAGAA	AGGATTTGCT	GGATCTAAGC	2100
ACCAATAGAA	ATCAATTTGT	GGATGCATTT	GGTAGTCTTA	TGGATGATTT	GGGTGCTGTT	2160
GGGCAGACAG	TTGTAAATGC	TGTAAGTGGT	GTGGCTACGC	TGTTTAGCTC	AATTGTAACA	2220
GGATTTATTA	ATTTTCATTAA	AAACCCATTT	GGTGGAATGT	TAATGATTAT	TGTTGTTATT	2280
GGTGTGCTAT	TTGCCATCTA	CTTCTTGACC	AAAAAGACGA	AGATATATGA	GACGGCACCG	2340
ATTAAGATGA	TTTATCCTGA	AATTGACAAG	CTGAAAGAAC	GTGAGGGAAA	ATCAGAAAATA	2400
GCACCAATCA	GTGAAGAAGA	GCTGGAGAGA	ATTGTACTTG	CTATGCATAT	CCATCAACAA	2460
AATTCACATA	TGGAACAAA	AACAAGGAAG	GATCCCAAAG	ACAGCATATT	AAACAAGGGCA	2520
CAAAATATGC	TACGCAAAAG	ATCAGGATAT	TCTAATTTAA	AAAATGCTGA	ATCTGTGGAG	2580
ATGTTAAACA	CTTTTATAA					2598

Figure 3

MAGSLKLRGS	VLALWYLYQV	ALYSLSIAET	GVTSPNTAT	WSTESPLTGH	50
YGTHDSSHGE	RGNNENRDSE	EQNKNIYGSP	STFPYRVCSA	SGVGDVFRFQ	100
TDHVCPDASD	MVHSEGILLI	YKQNIIPFMF	RVRKYRKVVT	TSTVYNGIYS	150
DSITNQHTFY	KSIEPWETEK	MDTIYQCFNS	LRLNTGGNLL	TYVDRDDINM	200
TVFLQPVDGV	TPDVKRYGSQ	PELYLEPGWF	WGSYRRRTTV	NCELMDMFAR	250
SNPPFDFFVT	ATGDTVEMSP	FWSGEDDHEN	KMHEKPWFVS	VINNYKVVDY	300
QNRGTVPLGK	TRIFLDREEY	TLSWEKHLKN	MSYCPLTLWK	AFYNGIQTEH	350
SGSYHFVAND	ITASFTTSKE	DMKEFNNTYH	CLNEEIKAEI	EKKYAKVNST	400
HSKYGDLKYF	KTDGGLYLVW	QPLIQNRLLD	AKNKLNNETY	SRRSRRQAES	450
TTDPMMEMTG	NGAGGEYSSE	NSITVAQVQY	AYDNLIRIN	NILEDLSKAW	500
CREQHRAALV	WNELSKINPT	SVMSMIYNRP	VSAKRIGDVI	SVSNCIVVDQ	550
TSVSLHKSLR	LLSASDEKCF	SRPPVTFKFM	NDSTIYKGQL	GVNNEILLTT	600
TYLETCQENT	EYYFQAKTDM	YIYKNYEHLK	TVPLSSITTL	DTFIALNFTL	650
LENVDFKVIE	LYTRDEKRLS	NVFDIETMFR	EYNYYAQRVS	GLRKDLLDLS	700
TNRNQFVDAF	GSLMDDLGA	GQTVVNAVSG	VATLFSSIVT	GFINFIKNPF	750
GGMLMIIVVI	GVLFAIYFLT	KKTKIYETAP	IKMIYPEIDK	LKEREGKSEI	800
APISEEEELER	IVLAMHIHQQ	NSHMETKTRK	DPKDSILTRA	QNMLRKRSKY	850
SNLKNAESVE	MLNTL				865

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Figure 4

pGHV-gpB DNA.txt	-----AATCT	TCGTATCAGA	ATAAATAACA	25
pGHV1 DNA. (641-1300)	CGCCGCCGTC	CGGCTCCACG	GTGGTGCGGC	688
		T G C GA	A C	
pGHV-gpB DNA.txt	TTTTGGAAGA	TTTGTCAAAG	GCATGGTGTC	75
pGHV1 DNA. (641-1300)	GCCCCGAGTA	CTCG-CAGGG	GCGCAACTTC	737
	GA A T G CA G GC	TC	G G A T G TGCT	
pGHV-gpB DNA.txt	CTGGTGTGGA	ATGAGCTCAG	CAAGATTAAT	125
pGHV1 DNA. (641-1300)	CT----T-CA	AGGAGAACAT	C--G-CC--C	776
	CT T A A GAG CA	C G	C CACAAG TCA G C	
pGHV-gpB DNA.txt	GATTTACAAT	-AGACCCGTA	TCAGC-CAAA	172
pGHV1 DNA. (641-1300)	CATCTACTAC	AAGAAGCTCA	TCGTACAGAC	826
	AT TAC A	AGA C A	TC C C A G T G G CA T	
pGHV-gpB DNA.txt	CAGTCTCTAA	C-TGTATTG-	-TGGTAGACC	219
pGHV1 DNA. (641-1300)	ACGCGGCCAT	CACGAACCGC	TTCACAGACC	876
	G C A C G A G T	AGACC	GT C C T CA	
pGHV-gpB DNA.txt	AAAAGTCTCA	GGCTTCTCAG	TGCATCGGAT	269
pGHV1 DNA. (641-1300)	GAGA-TCACG	GACGTGATCG	ACCGCCG--C	922
	A A TC C C T G	C CG	G AAGTC TCTC A A	
pGHV-gpB DNA.txt	TCCAGTGACA	T--TTAA-GT	TTATGA-ATG	314
pGHV1 DNA. (641-1300)	CCGAGT-ACG	TGCGCAACAA	CCACAAGGTG	971
	C AGT AC T AA	A A TG	AC G T C AG	
pGHV-gpB DNA.txt	GCAACTAG--	GAGTCAATAA	TGAGATTCT-	354
pGHV1 DNA. (641-1300)	GAACCCCGTC	GAGGTGGACC	TGCGCCCTC	1021
	G A C GAG	TG G CT	CT AAC C C	
pGHV-gpB DNA.txt	TAC-C--TTG	AAACA-TGTC	-AGGAAA---	395
pGHV1 DNA. (641-1300)	CCCGCGGCTG	GCACACCACC	AACGACACCT	1071
	C C TG	ACA C	A GA A ACAC AG C C	
pGHV-gpB DNA.txt	GGCAAAGACA	GACATGTACA	TTTACAAAAA	439
pGHV1 DNA. (641-1300)	GGCTTCTAC-	CACACGGGCA	CCTCCGTCAA	1120
	GGC AC	ACA G CA	T C AA CT AT GAG A TG	
pGHV-gpB DNA.txt	AGAC-----	--TGTGCCTT	TA-----TCT	476
pGHV1 DNA. (641-1300)	AGGCGCGCTC	CGTGTACCCC	TACGACTCCT	1170
	AG C	TGT CC	TA CT TCG C CAC G AC	
pGHV-gpB DNA.txt	ATT---TATA	GCCCTTAATT	TTAC--ACTA	521
pGHV1 DNA. (641-1300)	ATTGTGTACA	TGTCCCCCTT	CTACGGCCTG	1220
	ATT TA A C TT	TAC T	GAG G AC A	
pGHV-gpB DNA.txt	AGTCATTGAA	CTTTATACCA	GGG----ACG	564
pGHV1 DNA. (641-1300)	GCACATCG-G	CTACGCGCCC	GGGCGCTTCC	1269
	CAT G CT	CC	GGG C AG G GG A TA A	
pGHV-gpB DNA.txt	GTCTTTGACA	TTGAAACAAT	G-----	585
pGHV1 DNA. (641-1300)	CCCATCGAC-	CTGGACTCGC	GCCTCCGCGC	1300
	C T GAC	TG A G		

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[illegible]

Figure 7

pGHV-gpB prot	NLRIRINNIL EDLSKAWCRE QHRAALVWNE LSKINPTSVM SMIYNRPVSA	50
pGHV2 prot.txt	S--IMIANNL -----C-- --YSTLI--- LNDEDVTG-- -----IDE	25
	I I N L C L L T	
pGHV-gpB prot	KRIGDVISVS NCIVVDQTSV SLHKSLRLLS ASDEKCFSRP PVTFKFMNDS	100
pGHV2 prot.txt	K---DILTVH ---VNKNTV-----YRFVRSS	45
	K D V V V F S	
pGHV-gpB prot	---TIYKGQL GV-NNBILLT TTYLSTCOEN TEYFFQAKTD MYI---YKN-	142
pGHV2 prot.txt	VRESILGTLT SRWLRKRKEV KARMKRCEDP MLALILDKQQ LALKVTCNAF	95
	I L C K	
pGHV-gpB prot	YEHLKTVP-- LSSITTLDTF IALNFTLL-E NVDFKVIELY TRD---EK-R	185
pGHV2 prot.txt	YGFTGAVHGL LPCLPLAASI TSIGRDMRLQ TSDFINNVLS SREYVSEKFS	145
	Y V L L DF L R EK	
pGHV-gpB prot	LSNV-F--DI ETM-	195
pGHV2 prot.txt	LSDGDFQGDF SPEC	159
	LS F D	

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Figure 8

pGHV-gpB DNA	AATCTTCGTA TCAGAATAAA TAACATTTTG GAAGATTGTG CAAAGGCATG	50
AF118399 DNA.txt	-----	
pGHV-gpB DNA	GTGTCGTGAG CAGCATAGAG CTGCTCTGGT GTGGAATGAG CTCAGCAAGA	100
AF118399 DNA.txt	-----	
pGHV-gpB DNA	TTAATCCCAC AAGCGTCATG AGCATGATTT ACAATAGACC CGTATCAGCC	150
AF118399 DNA.txt	-----	
pGHV-gpB DNA	AAAAGAATAG GAGATGTCAT TTCAGTCTCT AACTGTATTG TGGTAGACCA	200
AF118399 DNA.txt	-----	
pGHV-gpB DNA	AACCAGTGTC TCATTACATA AAAGTCTCAG GCTTCTCAGT GCATCGGATG	250
AF118399 DNA.txt	-----	
pGHV-gpB DNA	AAAAGTGCTT CTCTAGACCT CCAGTGACAT TTAAGTTTAT GAATGACAGT	300
AF118399 DNA.txt	-----	14
	T AT ATG CA T	
pGHV-gpB DNA	ACTATTTACA AAGGGCAACT AGGA-GTCAA TAATGAGATT CTCTTAACCA	349
AF118399 DNA.txt	-CTACCC-TA ATCCATCATG AAGACCTGCA TAAATATCCT CAATTAAGG	62
	CTA A A A A GA T A TAA A T A TTAA	
pGHV-gpB DNA	CAACATACCT TGAAACATGT CAGGAAAAACA CTGAGTATTA CTTTCAGGCA	399
AF118399 DNA.txt	AGGAGGATTA TGAAACAT--	83
	A TGAAACAT TTT	
pGHV-gpB DNA	AAGACAGACA TGTACATTTA CAAAAACTAT GAGCATTGTA AGACTGTGCC	449
AF118399 DNA.txt	-----	95
	TG---ATT-- -AG---TT-- ---CTG---	
	TG ATT AG TT CTG	
pGHV-gpB DNA	TTTATCTTCG ATCACCACAC TAGATACATT TATAGCCCTT AATTTTACAC	499
AF118399 DNA.txt	-----	99
	-----GTCC--	
	GTCC	
pGHV-gpB DNA	TATTGGAGAA TGTGACTTTT -----AAAG TCAT-T--GA A---CTT---	534
AF118399 DNA.txt	-----	139
	TGTTCACTTT GTAAAAAAAC ACATATCAGA ATCTCTTCTG	
	TGTT ACTTT AAA CAT T GA A CTT	
pGHV-gpB DNA	--TA----- -TAC--CA-- G--GG--ACG AGA----- --AG--AGG-	555
AF118399 DNA.txt	TCTAACCTGC TTACAACATG GCTGGCTAAG AGAAAAATGA TCAGAAAGGA	189
	TA TAC CA G GG A G AGA AG AGG	
pGHV-gpB DNA	CTTAGTA--A TGT-CT--TT GACA-TTGA- AACAAATG----	585
AF118399 DNA.txt	ATTAGCAGCA TGTGCTGACC CAAAGCTCAG GACAAT-TTT AGATAAACAG	238
	TTAG A A TGT CT A A T A ACAAT	
pGHV-gpB DNA	-----	585
AF118399 DNA.txt	CAGCTTGCAA TTAAGGTGAC ATGCAATGCT GTGTATGGGT TCACTGGTGT	288
pGHV-gpB DNA	-----	585
AF118399 DNA.txt	TGCATCTGGT ATGCTGCCCT GTCTCAAGAT TGCAGAGACC ATAACATATGC	338
pGHV-gpB DNA	-----	585
AF118399 DNA.txt	AAGGAAGGGC CATGTTGGAA AAGACAAAAG TATTTGTAGA GAATTTAAGT	388
pGHV-gpB DNA	-----	585
AF118399 DNA.txt	CATGAGGATC TCCATTCCAT CTGTAAGGTT GGCTTTATGC CTCAGTCACC	438
pGHV-gpB DNA	-----	585
AF118399 DNA.txt	AAACAGCATT GATAAACCTT TCAAGGTG	466

Figure 9

pGHV-gpB DNA	-----	-----	-----	-----	-----	50
AF118401 DNA.txt	GAGGACCTGC	ATAAGTATCC	TCAATTAAAG	GAGGATGATT	ATGAAACATT	
pGHV-gpB DNA	-----	-----	-----	---AATCTTC	GTATCAGAAT	17
AF118401 DNA.txt	TTTGATTAGT	TCTGGCCCTG	TTCACCTTTGT	AAAAAAACAC	ATATCAGAAT	100
				AA	C TATCAGAAT	
pGHV-gpB DNA	AAATAACATT	TTGGAAGATT	TGTCAAAGGC	ATGGTGTCTG	GAGCAGCATA	67
AF118401 DNA.txt	-----C-TC	TT-----	-----	-----	-----	105
	C T	TT				
pGHV-gpB DNA	GAGCTGCTCT	GGTGTGGAAT	GAGCTCAGCA	AGATTAATCC	CACAAGCGTC	117
AF118401 DNA.txt	---CTG-TC-	TT---GAA-	---CTT---	-G-----CT	CACAA---C	125
	CTG TC	GAA	CT	G	C CACAA C	
pGHV-gpB DNA	ATGAGCATGA	TTTACAATAG	ACCCGTATCA	GCCAAAAGAA	-----T---	158
AF118401 DNA.txt	ATG-GC-TG-	-----	-----	GCCAAGAGAA	AAATGATCAG	152
	ATG GC TG				T	
pGHV-gpB DNA	--AGG-----	--AG-ATGT-	-----	-----CA	--TTT-----	172
AF118401 DNA.txt	AAAGGAATTG	ACAGCATGTG	CTGATCCAAA	GCTCAGGACA	ATTTTAGATA	202
	AGG	AG ATGT		CA	TTT	
pGHV-gpB DNA	-----CAGTC	T-----CTA--	---AC-TGTA	TTG-TG-GTA	--GA-CCA--	200
AF118401 DNA.txt	AACAGCAGCT	TGCAATTAAG	GTGACATGCA	ATGCTGTGTA	TGGATTCACT	252
	CAG	T TA	AC TG A	TG TG GTA	GA CA	
pGHV-gpB DNA	-----A-	-----AC-CA	G---TGTCTC	A-----	-----TTAC	217
AF118401 DNA.txt	GGTGTTCAT	CTGGTATGCT	GCCATGTCTC	AAGATTGCAG	AGACCATCAC	302
	A	A C	G TGTCTC	A	TCAC	
pGHV-gpB DNA	-----	-----	-----AT	AAAAGT--CT	-CAG-GCTTC	235
AF118401 DNA.txt	TATGCAAGGA	AGGGCCATGT	TGGAAAAGAC	AAAAGTATTT	GTAGAGAATC	352
			A	AAAAGT	T AG G TC	
pGHV-gpB DNA	TCAG---TGC	A----TCGGA	T-GAAAAGT-	-GCTT--CTC	TAGACCTCCA	273
AF118401 DNA.txt	TGAGTCATGA	AGATCTCCGT	TCCATATGTA	AGGTTGGCTC	TATACCTC-A	401
	T AG TG A	TC G T A A GT	G TT CTC	TA ACCTC A		
pGHV-gpB DNA	GTGACATTTA	AGTTTATGAA	TGACAGTACT	ATTTACAAAG	GGCAACTAGG	323
AF118401 DNA.txt	GT--CA-TCA	A---ACG--	TG-----	-TTT-----	-----	417
	GT CA T A A	A G	TG	TTT		
pGHV-gpB DNA	AGTCAATAAT	GAGATTCTCT	TAACCACAAC	ATACCTTGAA	ACATGTCAGG	373
AF118401 DNA.txt	-G---ATAAA	-----	-----	-----	-----	423
	G ATAA					
pGHV-gpB DNA	AAAACACTGA	GTATTACTTT	CAGGCAAAGA	CAGACATGTA	CATTTACAAA	423
AF118401 DNA.txt	-----	-----	-----	-----	-----	423
pGHV-gpB DNA	AACTATGAGC	ATTTGAAGAC	TGTGCCTTTA	TCTTCGATCA	CCACACTAGA	473
AF118401 DNA.txt	-----	-----	-----	-----	-----	423
pGHV-gpB DNA	TACATTTATA	GCCCTTAATT	TTACACTATT	GGAGAATGTT	GACTTTAAAG	523
AF118401 DNA.txt	-----	-----	-----	-----	-----	423
pGHV-gpB DNA	TCATTGAACT	TTATACCAGG	GACGAGAAGA	GGCTTAGTAA	TGTCCTTGAC	573
AF118401 DNA.txt	-----	-----	-----	-----	-----	423
pGHV-gpB DNA	ATTGAAACAA	TG	585			
AF118401 DNA.txt	-----	--	423			

Figure 6. The effect of the number of iterations on the accuracy of the proposed algorithm. The figure shows two plots side-by-side. The left plot shows the accuracy of the proposed algorithm (in %) versus the number of iterations (from 0 to 100). The right plot shows the accuracy of the proposed algorithm (in %) versus the number of iterations (from 0 to 100).

Score = 91.1 bits (47), Expect = 7e-16
Identities = 117/152 (76%), Positives = 117/152 (76%)

```

Query:      1498  tgggtgctcgtgagcagcatagagctgctctgggtgtggaatgagctcagcaagattaatccc 1557
             ||||| |||||||||||| |||| |||| |||||| |||||| ||||| |||||
Sbjct:      18194 tggtgccgtgagcagcaccgagcctctctcatgtggaacgagctaagcaaaatcaaccct 18253

Query:      1558  acaagcgtcatgagcatgattacaatagaccgatatcagccaaaagaataggagatgtc 1617
             || || || |||||| || |||| | || |||||| |||||||||| ||||||||
Sbjct:      18254 accagtgtgatgagctctatatacggggcgccagtatctgccaaaagaattggagatgtg 18313

Query:      1618  atttcagtctctaactgtattgtggttagacca 1649
             || || |||||| ||||| | |||| |||||
Sbjct:      18314 atatctgtctctcactgtgtggtggtggacca 18345

```

Figure 11(a)

gi|2337975 (AF005370) glycoprotein B [Alcelaphine herpesvirus 1]
Length = 854

Score = 953 bits (2437), Expect = 0.0

Identities = 463/804 (57%), Positives = 589/804 (72%), Gaps = 26/804 (3%)

Query: 74 KNIYGSPSTFPYRVCSASGVGDVFRFQTDHVCPCDASDMVHSEGILLIYKQNIIPFMFRVR 133
K I+ PS FP+RVCSAS +GD+FRFQT H CP+ D H+EGILLI+K+NI+P++F+VR
Sbjct: 55 KGIHSDPSAFPFRVCSASNIGDIFRFQTSHCPCNTKDKHEGILLIFKENIVPYVFKVR 114

Query: 134 KYRKVTTSTVYNGIYSDSITNQHTFYKSIEPWETEKMDTIYQCFNSLRLNTGGNLLTYV 193
KYRK+VTTST+YNGIY+D++TNQH F KS+ +ET +MDTIYQC+NSL + GGNLL Y
Sbjct: 115 KYRKIVTTSTIYNGIYADAVTNQHVFSKSVPIYETRRMDTIYQCYNSLDVTVGNNLLVYT 174

Query: 194 DRDDINMTVFLQPVGDVTPDVKRYGSQPELYLEPGWFGWSYRRRTTVNCELMDMFARSNP 253
D D NMTV LQPVGD++ V+RY SQPE++ EPGW G YRRRTTVNCE+ + AR+ P
Sbjct: 175 DNDGSNMTVDLQPVGDGLSNSVRRYHSQPEIHAEPGWLLGGYRRRTTVNCEVTETDARAVP 234

Query: 254 PFDFEVTATGDTVEMSPFWSGEDDHENKMHEKPWFVSVINNYKVVDYQNRGTVPGLKTRI 313
PF +F+T GDT+EMSPFWS + E ++V +Y+VVDY+ RGT P G TRI
Sbjct: 235 PFRYFITNIGDTIEMSPFWSKAWNTEFSGEPDRTLTVAKDYRVVDYKFRGTQPPQHTRI 294

Query: 314 FLDREYYTLSEWKLKNSYCPLTLWKAFYNGIQTEHSGSYHFVANDITASFTTSKEDMK 373
F+D+EEYTLSEW + +N+SYC WK+F N I+TEH S HFVANDITASF T +
Sbjct: 295 FVDKEEYTLSEWQAFRNISYCRWAHWKSFDAIKTEHGKSLHFVANDITASFYTPNTQTR 354

Query: 374 EFNTTYHCLNXXXXXXXXXXXXXXXXXVNSTHSHYKGLKYFKTDGGLYLWVQPLIQNRLLDAKN 433
E + CLN VN THS G +Y+ T+GGL LVWQPL+Q +LLDAK
Sbjct: 355 EVLGKHVCLNNTIESELKSRLAKVNDTHSPNGTAQYYLTNGGLLLWVQPLVQQLLLDAKG 414

Query: 434 KLN-----NETYSRRSRRQAESTTDPMMEMTGNGAGGEYSSENSITVAQVQYAYDN 484
L+ T + RSRRQ S + +G Y++E++I + Q+Q+AYD
Sbjct: 415 LLDVAVKKQNTTTTTTTTTTSRRRQRRSVS-----SGIDDVYTAESTILLTQIQFAYDT 466

Query: 485 LRIRINNILEDLKAWCREQHRAALVWNELSKINPTSVMSMIYNRPVSAKRIGDVISVSN 544
LR +INN+LE+LS+AWCREQHRA+L+WNELSKINPTSVMS IY RVPVSAKRIGDVISVS+
Sbjct: 467 LRAQINNVLLELSRAWCREQHRAALVWNELSKINPTSVMSIYGRPVSAKRIGDVISVSH 526

Query: 545 CIVVDQTSVSLHKSRLRLLSA-SDEKCFSRPPVTFKFMNDSTIYKQGLGVNNEILLTTTYL 603
C+VVDQ SVSLH+S+R+ +C+SRPPVTFKF+NDS +YKQGLGVNNEILLTTT +
Sbjct: 527 CVVVDQDSVSLHRSRMRVPGRDKTHECYSRPPVTFKFINDSHLYKQGLGVNNEILLTTTAV 586

Query: 604 ETCQENTTEYFQAKTDMYIYKNYHLKTVPLSSITTLDTFIALNFTLLENVDFKVIELYT 663
E C ENTE+YFQ +MY YKNY H+KT+P+ + TLDTF+ LN TL+EN+DF+VIELY+
Sbjct: 587 EICHENTEYFQGGNNMYFYKNYRHVKTMPVGDVATLDTFMVLNLTLENIDFQVIELYS 646

Query: 664 RDEKRLSNVFDIETMFREYNYYAQRVSGLRKDLDDLSTNRNQFVDAFGSLMDDLGVAVGQT 723
R+EKR+S FDIETMFREYNYY QRV+GLR+DL DL+TNRNQFVDAFGSLMDDLGV+T
Sbjct: 647 REEKRMSAFDIETMFREYNYYTQRVTLRRDLTDLATNRNQFVDAFGSLMDDLGVVGKT 706



```
Query: 724 VVNAVSGVATLFSSIVTGFINFIKNPFGGMLMIIVVIGVLF AIYFLT KTKTIYETAPIKM 783
      V+NAVS VATLFSSIV+G INFIKNPFGGML+ ++ V+ + L +K K + P++M
Sbjct: 707 VLNAVSSVATLFSSIVSGIINFIKNPFGGMLLFGLIAAVVITVILLNRKAKRFAQNPVQM 766

Query: 784 IYPEIDKLKEREGKSEIAPISEEEELERIVLAMHIHQONSHMETK-----TRKDPKDSI 836
      IYP+I + + + ++ PIS+ EL+RI+LAMH + + E+K T P D
Sbjct: 767 IYPDIKTITSQREELQVDPISKHELDRIMLAMHDYHASKQPESKQDEEQGSTTSGPAD-W 825

Query: 837 LTRAQNMLLRKRSYGYNLKN AESVE 860
      L +A+N+LR+R+GY LK +S E
Sbjct: 826 LNKAKNVLRRRAGYKPLKRTDSFE 849
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